

Davis, Minh-Tam

From: Davis, Minh-Tam
Sent: Monday, January 09, 2006 4:08 PM
To: Chan, Christina
Subject: Rush search request for 10/048046

1) Please search in commercial database, issued patent files and PGPUB:

A nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

2) Interference search only for:

- a) SEQ ID NO:1
- b) oligonucleotide search for SEQ ID NO:1, with size limitation for the sequences in the database to equal or less than 50 nucleotides.
- c) A nucleic acid encoding SEQ ID NO:2.
- d) oligonucleotide search for a nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

Thank you.

MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

GenCore version 5.1.6
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OM protein - nucleic acid search, using frame_plus_p2n model

Run on: January 12, 2006, 07:58:47 / Search time 316 Seconds

(without alignments)
3735.130 Million cell updates/sec

Title: US-10-048-046-2

Perfect score: 664

Sequences: 1 MERPEKSGKSPPOPMGRLL.....VKAHAKKFNHCCEOTRFKN 664

Scoring table:

Xgapop 60.0	Xgapext 60.0
Ygapop 60.0	Ygapext 60.0
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1293591

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame_plus_model -DEV=rlh
-O=/cg2_1/USPTO_SPOOL/US10048046/runat_10012006_122939_24142/app_query.fasta_1.839
-DB=Issued_Patents_NA -QFMT=fastap -SUPFIX=011g_sz50.rn1 -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=011g
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50
-USER=US10048046@CGN_1_1_193@runat_10012006_122939_24142 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBIOCK=100 -LONGLIOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA:

- 1: /cg2_6/prodata/1/lna/1_COMB.seq:*
- 2: /cg2_6/prodata/1/lna/5_COMB.seq:*
- 3: /cg2_6/prodata/1/lna/5A_COMB.seq:*
- 4: /cg2_6/prodata/1/lna/5B_COMB.seq:*
- 5: /cg2_6/prodata/1/lna/6_COMB.seq:*
- 6: /cg2_6/prodata/1/lna/6CTUS_COMB.seq:*
- 7: /cg2_6/prodata/1/lna/6P_COMB.seq:*
- 8: /cg2_6/prodata/1/lna/6B_COMB.seq:*
- 9: /cg2_6/prodata/1/lna/Backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.1	25	US-09-396-196G-104092	Sequence 104092,
2	7	1.1	25	US-09-396-196G-104100	Sequence 104100,
3	7	1.1	25	US-09-396-196G-104101	Sequence 104101,
4	7	1.1	25	US-09-396-196G-104102	Sequence 104102,
5	7	1.1	25	US-09-396-196G-104103	Sequence 104103,
6	7	1.1	30	US-08-078-683A-35	Sequence 35, Appl
7	7	1.1	30	US-08-471-970A-35	Sequence 35, Appl
8	7	1.1	30	US-09-723-677B-35	Sequence 35, Appl
9	7	1.1	33	US-08-196-538-16	Sequence 16, Appl

10	7	1.1	35	US-08-582-740-6	Sequence 6, Appl1
11	7	1.1	35	US-09-109-879-6	Sequence 6, Appl1
12	7	1.1	39	US-08-582-740-63	Sequence 63, Appl1
13	7	1.1	39	US-09-109-879-63	Sequence 63, Appl1
14	7	1.1	40	US-07-931-473B-77	Sequence 77, Appl1
15	7	1.1	40	US-07-931-473B-109	Sequence 109, Appl
16	7	1.1	40	US-07-714-131C-77	Sequence 77, Appl
17	7	1.1	40	US-07-714-131C-109	Sequence 109, Appl
18	7	1.1	40	US-08-412-110-77	Sequence 77, Appl
19	7	1.1	40	US-08-412-110-109	Sequence 109, Appl
20	7	1.1	40	US-08-409-442A-77	Sequence 77, Appl1
21	7	1.1	40	US-08-409-442A-109	Sequence 109, Appl
22	7	1.1	40	US-08-469-609A-77	Sequence 77, Appl
23	7	1.1	40	US-08-469-609A-109	Sequence 109, Appl
24	7	1.1	40	US-09-143-190-77	Sequence 77, Appl
25	7	1.1	40	US-09-143-190-109	Sequence 109, Appl
26	7	1.1	40	US-09-502-344-77	Sequence 77, Appl
27	7	1.1	40	US-09-502-344-109	Sequence 109, Appl
28	7	1.1	40	US-10-037-986-77	Sequence 77, Appl
29	7	1.1	40	US-10-037-986-109	Sequence 109, Appl
30	7	1.1	50	US-09-849-069-15	Sequence 15, Appl
31	7	1.1	50	US-10-131-827-5920	Sequence 5920, Ap
32	6	0.9	18	US-08-311-486C-1074	Sequence 1074, Ap
33	6	0.9	18	US-08-311-486C-1141	Sequence 1141, Ap
34	6	0.9	18	US-09-422-978-10937	Sequence 10937, A
35	6	0.9	18	US-10-620-049-3	Sequence 3, Appl1
36	6	0.9	19	US-09-352-654A-31	Sequence 31, Appl
37	6	0.9	19	US-09-348-097-31	Sequence 31, Appl
38	6	0.9	19	US-09-350-275-31	Sequence 31, Appl
39	6	0.9	19	US-09-909-558-31	Sequence 31, Appl
40	6	0.9	20	US-08-770-565-3	Sequence 3, Appl1
41	6	0.9	20	US-08-964-725-12	Sequence 12, Appl
42	6	0.9	20	US-08-833-377-7	Sequence 7, Appl1
43	6	0.9	20	US-08-281-203-3	Sequence 3, Appl1
44	6	0.9	20	US-09-166-186-25	Sequence 25, Appl
45	6	0.9	20	US-09-313-932-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-396-196G-104092/c
Sequence 104092, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104092
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-104092

Alignment Scores:

Pred. No.: 148
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.05%
DB: 3
Gaps: 0
Length: 25
Matches: 7
Mismatch: 0
Indels: 0
US-10-048-046-2 (1-664) x US-09-396-196G-104092 (1-25)

Qy 18 ArgLeuLeuArgLeuGlyAla 24
 DB 25 AGATTGCTCAGATTGGCGCT 5

RESULT 2
 US-09-396-196G-104100/c
 / Sequence 104100, Application US/09396196G
 / Patent No. 6821724

GENERAL INFORMATION:
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack
 / APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.
 / TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
 / CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17
 / NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 104100

LENGTH: 25
 / TYPE: DNA

ORGANISM: mus musculus
 / US-09-396-196G-104100

Alignment Scores:
 Pred. No.: 148
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 3

US-10-048-046-2 (1-664) x US-09-396-196G-104100 (1-25)
 Qy 18 ArgLeuLeuArgLeuGlyAla 24
 DB 24 AGATTGCTCAGATTGGCGCT 4

RESULT 3
 US-09-396-196G-104101/c
 / Sequence 104101, Application US/09396196G
 / Patent No. 6821724

GENERAL INFORMATION:
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack
 / APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.
 / TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
 / CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17
 / NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 104101

LENGTH: 25
 / TYPE: DNA

ORGANISM: mus musculus
 / US-09-396-196G-104101

Alignment Scores:
 Pred. No.: 148
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 3

Qy 18 ArgLeuLeuArgLeuGlyAla 24
 DB 23 AGATTGCTCAGATTGGCGCT 3

RESULT 4
 US-09-396-196G-104102/c
 / Sequence 104102, Application US/09396196G
 / Patent No. 6821724

GENERAL INFORMATION:
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack
 / APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.
 / TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
 / CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17
 / NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 104102

LENGTH: 25
 / TYPE: DNA

ORGANISM: mus musculus
 / US-09-396-196G-104102

Alignment Scores:
 Pred. No.: 148
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 3

US-10-048-046-2 (1-664) x US-09-396-196G-104102 (1-25)
 Qy 18 ArgLeuLeuArgLeuGlyAla 24
 DB 22 AGATTGCTCAGATTGGCGCT 2

RESULT 5
 US-09-396-196G-104103/c
 / Sequence 104103, Application US/09396196G
 / Patent No. 6821724

GENERAL INFORMATION:
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack
 / APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.
 / TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
 / CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17
 / NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 104103

LENGTH: 25
 / TYPE: DNA

ORGANISM: mus musculus
 / US-09-396-196G-104103

Alignment Scores:
 Pred. No.: 148
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 3

US-10-048-046-2 (1-664) x US-09-396-1966-104103 (1-25)

Qy 18 ArgleuleuArgleuGlyAla 24
|||||
Db 21 AGATTGCTCAATTGGGCGCT 1

RESULT 6

US-08-078-683A-35/c
Sequence 35, Application US/08078683A
Patent No. 5486599
GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Kato, Masao
TITLE OF INVENTION: Construction and Use of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078, 683A
FILING DATE: 17-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CME-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-078-683A-35

Alignment Scores:

Pred. No.:	177	Length:	30
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	2	Gaps:	0

US-10-048-046-2 (1-664) x US-08-078-683A-35 (1-30)

Qy 623 SerGluLeuProValAlaVal 629
|||||

Db 26 TCCGAGTTGCCGTTGCCAGTC 6

RESULT 7

US-08-471-970A-35/c
Sequence 35, Application US/08471970A
Patent No. 6531295
GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Kato, Masao
TITLE OF INVENTION: Construction and Use of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471, 970A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078, 683
FILING DATE: 17-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CME-062DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-471-970A-35

Alignment Scores:

Pred. No.:	177	Length:	30
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	3	Gaps:	0

US-10-048-046-2 (1-664) x US-08-471-970A-35 (1-30)

Qy 623 SerGluLeuProValAlaVal 629
|||||

Db 26 TCCGAGTTGCCGTTGCCAGTC 6

RESULT 8

US-09-723-677B-35/c
Sequence 35, Application US/09723677B
Patent No. 6699968
GENERAL INFORMATION:
APPLICANT: SAUNDERS, SCOTT
APPLICANT: BERNFIELD, MERTON
APPLICANT: KATO, MASAO
TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
TITLE OF INVENTION: 101353-151
CURRENT APPLICATION NUMBER: US/09/723, 677B
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 08/471, 970
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/078, 683
PRIOR FILING DATE: 1993-06-17
PRIOR APPLICATION NUMBER: 07/856, 869
PRIOR FILING DATE: 1992-03-24
PRIOR APPLICATION NUMBER: 07/757, 654
PRIOR FILING DATE: 1991-09-06
PRIOR APPLICATION NUMBER: 07/746, 797
PRIOR FILING DATE: 1991-08-12
PRIOR APPLICATION NUMBER: 07/331, 585

PRIOR FILING DATE: 1989-03-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 30
TYPE: DNA
ORGANISM: MUS BP
US-09-723-677B-35

Alignment Scores:
Pred. No.: 177 Length: 30
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-723-677B-35 (1-30)

Cy 623 SerGiuleuProValAlaVal 629
DB 26 TCCGAGTCCGATTCGATC 6

RESULT 9
US-08-196-538-16
Sequence 16, Application US/08196538
Patent No. 5639608
GENERAL INFORMATION:
APPLICANT: Stanley Tabor
APPLICANT: Charles C. Richardson
TITLE OF INVENTION: USE OF SHORT OLIGONUCLEOTIDES AS PRIMERS
TITLE OF INVENTION: FOR DNA SEQUENCING
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,538
FILING DATE: February 14, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/985,468
FILING DATE: December 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/0930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-196-538-16

Alignment Scores:
Pred. No.: 193 Length: 33
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.05% Indels: 0
DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-08-196-538-16 (1-33)

Cy 159 ProArgValProProSerSer 165
DB 6 CCGAGATTCACCTTCCTCG 26

RESULT 10
US-08-582-740-6
Sequence 6, Application US/08582740
Patent No. 6037324
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: Inhibitors of MADCAM-1-Mediated
TITLE OF INVENTION: Interactions and Methods of Use Therefor
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,740
FILING DATE: 04-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-582-740-6

Alignment Scores:
Pred. No.: 205 Length: 35
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-08-582-740-6 (1-35)

Cy 207 GlySerGlyGlyGlyIle 213
DB 7 GGATCCGATGAGGAGGAGATT 27

RESULT 11
US-09-109-879-6
Sequence 6, Application US/09109879
Patent No. 6274556
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,879
FILING DATE: 02-JUL-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00291
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-109-879-6

Alignment Scores:
Pred. No.: 205 Length: 35
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-09-109-879-6 (1-35)

OY 207 GlySerGlyGlyGlyGlyLe 213
DB 7. GGATCCGGTGGAGGAGGATT 27

RESULT 12
US-08-582-740-63/C
Sequence 63, Application US/08582740
Patent No. 6037324
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: Inhibitors of MADCAM-1-Mediated
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESSES:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,740
FILING DATE: 04-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 1..39
US-08-582-740-63

Alignment Scores:
Pred. No.: 227 Length: 39
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-08-582-740-63 (1-39)

OY 207 GlySerGlyGlyGlyGlyLe 213
DB 24 GGATCCGGTGGAGGAGGATT 4

RESULT 13
US-09-109-879-63/C
Sequence 63, Application US/09109879
Patent No. 6274556
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,879
FILING DATE: 02-JUL-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00291
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..39
US-09-109-879-63

Alignment Scores:
Pred. No.: 227 Length: 39
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-109-879-63 (1-39)

OY 207 Glycerolglycylglycylle 213
DB 24 GCATCCGATCGAGGAGCAATT 4

RESULT 14
US-07-931-473B-77/c
Sequence 77, Application US/07931473B
Patent No. 5270163
GENERAL INFORMATION:
APPLICANT: Larry Gold
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSER: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-931-473B-77

Alignment Scores:
Pred. No.: 232 Length: 40
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-07-931-473B-77 (1-40)

OY 461 ProserTherServalserleu 467
DB 22 CTTTCGACATCCGAGACTTG 2

RESULT 15
US-07-931-473B-109/c
Sequence 109, Application US/07931473B
Patent No. 5270163
GENERAL INFORMATION:
APPLICANT: Larry Gold
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSER: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-931-473B-109

Alignment Scores:
Pred. No.: 232 Length: 40
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-07-931-473B-109 (1-40)

OY 461 ProserTherServalserleu 467
DB 22 CTTTCGACATCCGAGACTTG 2

Search completed: January 12, 2006, 10:59:56
Job time : 317 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2006, 10:50:02 | Search time 1360 seconds

(without alignments)
4037.402 Million cell updates/sec

Title: US-10-048-046-2

Perfect score: 664

Sequence: 1 MERPEKQSPPEPWGRL.....VKAHAKFNHCQTRFKN 664

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Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11076785

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:

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-DB=Published.Applications_NA_Main -QFMT=fastap -SUFFIX=colig_ssz50.rnpsm
-MINMATCH=0.1 -LOEPL=0 -LOEPL=0 -UNITS=bits -START=1 -END=1 -MATRIX=coligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORES=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=psic -NORM=ext -HEAPSIZ=500 -MINLEN=50
-USER=US10048046.ecen.1.1.1026 -runat_10012006_122940_24178 -NCPu=6 -ICPU=3
-NO MAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Published.Applications_NA_Main:

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2: /cgnt_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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5: /cgnt_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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9: /cgnt_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgnt_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.2	25	US-10-719-956-88030	Sequence 88030, A
2	8	1.2	25	US-11-036-317-24277	Sequence 24277, A
3	8	1.2	25	US-11-036-317-24394	Sequence 24394, A
4	8	1.2	25	US-11-036-317-60227	Sequence 60227, A
5	8	1.2	25	US-11-036-317-61246	Sequence 61246, A
6	8	1.2	25	US-11-036-317-67592	Sequence 67592, A
7	8	1.2	25	US-11-036-317-108822	Sequence 108822, A
8	8	1.2	25	US-11-036-317-131760	Sequence 131760, A

9	8	1.2	25	US-11-036-317-144618	Sequence 144618, A
10	8	1.2	25	US-11-036-317-153103	Sequence 153103, A
11	8	1.2	25	US-11-036-317-166836	Sequence 166836, A
12	8	1.2	25	US-11-036-317-198348	Sequence 198348, A
13	8	1.2	25	US-11-036-317-233307	Sequence 233307, A
14	8	1.2	25	US-11-036-317-259770	Sequence 259770, A
15	8	1.2	25	US-11-036-317-289125	Sequence 289125, A
16	8	1.2	25	US-11-036-317-320189	Sequence 320189, A
17	8	1.2	25	US-11-036-317-320979	Sequence 320979, A
18	8	1.2	25	US-11-036-317-364136	Sequence 364136, A
19	8	1.2	25	US-11-060-756-62495	Sequence 62495, A
20	8	1.2	25	US-11-060-756-62496	Sequence 62496, A
21	8	1.2	25	US-11-060-756-62497	Sequence 62497, A
22	8	1.2	25	US-11-060-756-62515	Sequence 62515, A
23	8	1.2	25	US-11-060-756-136129	Sequence 136129, A
24	8	1.2	25	US-11-060-756-152376	Sequence 152376, A
25	8	1.2	25	US-11-060-756-179266	Sequence 179266, A
26	8	1.2	25	US-11-060-756-184410	Sequence 184410, A
27	8	1.2	25	US-11-060-756-203366	Sequence 203366, A
28	8	1.2	25	US-11-060-756-203937	Sequence 203937, A
29	8	1.2	25	US-11-060-756-222359	Sequence 222359, A
30	8	1.2	25	US-11-060-756-225655	Sequence 225655, A
31	8	1.2	25	US-11-060-756-236413	Sequence 236413, A
32	8	1.2	25	US-11-060-756-279102	Sequence 279102, A
33	8	1.2	25	US-11-060-756-283375	Sequence 283375, A
34	8	1.1	22	US-10-032-585-5047	Sequence 5047, A
35	8	1.1	25	US-10-098-263B-61049	Sequence 61049, A
36	8	1.1	25	US-10-098-263B-61050	Sequence 61050, A
37	8	1.1	25	US-10-098-263B-61677	Sequence 61677, A
38	8	1.1	25	US-10-681-773-66621	Sequence 66621, A
39	8	1.1	25	US-10-681-773-66839	Sequence 66839, A
40	8	1.1	25	US-10-719-956-1889	Sequence 1889, A
41	8	1.1	25	US-10-719-956-34455	Sequence 34455, A
42	8	1.1	25	US-10-719-956-114291	Sequence 114291, A
43	8	1.1	25	US-10-719-956-114292	Sequence 114292, A
44	8	1.1	25	US-10-719-956-328012	Sequence 328012, A
45	8	1.1	25	US-10-719-956-328012	Sequence 328012, A

ALIGNMENTS

RESULT 1
US-10-719-956-88030
Sequence 88030, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 88030
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-88030

Alignment Scores:

Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25)

303 ThrcvclletleCysGlnapleu 310

|||||

Db 1

ACCTGTATCATCTGTCAAGACTT 24

RESULT 2

US-11-036-317-24277

Sequence 24277, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24277

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-24277

Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)

Cy 48 SerpHeProSerAnlyLeuVal 55

Db 1 TCTTCTTCCCGACATTAACGTC 24

RESULT 3

US-11-036-317-24394

Sequence 24394, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24394

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-24394

Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)

Cy 49 SerpHeProSerAnlyLeuVal 56

Db 2 TCTTCTTCCCGACATTAACGTC 25

RESULT 4

US-11-036-317-60227

Sequence 60227, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 60227

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-60227

Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)

Cy 49 SerpHeProSerAnlyLeuVal 56

Db 1 TCTTCTTCCCGACATTAACGTC 24

RESULT 5

US-11-036-317-61246

Sequence 61246, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 61246

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-61246

Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)

Cy 47 SerpHeProSerAnlyLeuVal 54

Db 2 GACCTCTTCTTCCCGACATTAAC 25

RESULT 6

US-11-036-317-67592

Sequence 67592, Application US/11036317
Publication No. US20050214823A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 67592
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-67592

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-67592 (1-25)

QY 46 CysApplUserPheProSerAen 53
DB 1 TGTGACCTCTCTTCCCGACGCAAT 24

RESULT 7
US-11-036-317-108822
/ Sequence 108822, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 108822
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-108822

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)

QY 388 AspMetLeuGlnProIlyValAlaArg 395
DB 1 GATATGCTGCAACCCAAAGTCAGG 24

RESULT 8
US-11-036-317-131760
/ Sequence 131760, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
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/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 131760
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-131760

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-131760 (1-25)

QY 492 MetProAspArgArgAlaGluArg 499
DB 2 ATGCTGACCGGAGAGCTGAACGG 25

RESULT 9
US-11-036-317-144618
/ Sequence 144618, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 144618
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-144618

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-144618 (1-25)

QY 413 AspValAspSerGlnUserSerAsp 420
DB 2 GATGTCGACGAGTAATCTCAGAT 25

RESULT 10
US-11-036-317-153103
/ Sequence 153103, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
```

```

CURRENT FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 153103
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-048-046-2 (1-664) x US-11-036-317-153103 (1-25)

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 10

US-10-048-046-2 (1-664) x US-11-036-317-153103 (1-25)

QY 405 ArgArgArgGlyCysAspLeuSer 412
DB 2 TCAGAGGAGCTGCTGACCTCTCT 25

RESULT 11
US-11-036-317-166836
Sequence 166836, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 166836
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-166836

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 10

US-10-048-046-2 (1-664) x US-11-036-317-166836 (1-25)

QY 42 ArgArgArgGlyCysAspLeuSer 49
DB 2 AGGAGAGAGGCTGCTGACCTCTCT 25

RESULT 12
US-11-036-317-198348
Sequence 198348, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13

```

```

NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 198348
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-198348

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 10

US-10-048-046-2 (1-664) x US-11-036-317-198348 (1-25)

QY 42 ArgArgArgGlyCysAspLeuSer 49
DB 1 AGGAGAGAGGCTGCTGACCTCTCT 24

RESULT 13
US-11-036-317-233307
Sequence 233307, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 233307
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-233307

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 10

US-10-048-046-2 (1-664) x US-11-036-317-233307 (1-25)

QY 559 IleLeuYaaNtyrLeuAlaThr 566
DB 2 ATCTGAAGATTACTGCGCAACC 25

RESULT 14
US-11-036-317-259770
Sequence 259770, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 259770

```

/ LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Mus musculus
 US-11-036-317-259770

Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-259770 (1-25)

QY 41 G|YATGATGATG|G|YCyAAp|leu 48
 |||||
 DB 2 GGAAAGAGAGAGAGCTGTGACCTC 25

RESULT 15

US-11-036-317-289125
 / Sequence 289125, Application US/11036317
 / Publication No. US20050214823A1
 / GENERAL INFORMATION:
 / APPLICANT: Williams, Alan
 / TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 / FILE REFERENCE: 3654.1
 / CURRENT APPLICATION NUMBER: US/11/036,317
 / CURRENT FILING DATE: 2005-01-13
 / PRIOR APPLICATION NUMBER: US 60/536,639
 / PRIOR FILING DATE: 2004-01-13
 / NUMBER OF SEQ ID NOS: 991174
 / SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 / SEQ ID NO 289125
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Mus musculus
 US-11-036-317-289125

Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-289125 (1-25)

QY 558 Ap|le|leu|y|A|B|E|T|Y|leu|A|A 565
 |||||
 DB 1 GACATCCTGAAGAAATTACCTGACA 24

Search completed: January 12, 2006, 13:54:49
 Job time : 1361 secs

Db 1 GGGGCGGGCGGGCGGGCGGU 21

RESULT 2

US-10-310-914A-638790/C
 / Sequence 638790, Application US/10310914A
 / Publication No. US20060003322A1
 / GENERAL INFORMATION:
 / APPLICANT: Bentwich, Isaac
 / APPLICANT: Shlier, Kyuzat
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 / TITLE OF INVENTION: uses thereof
 / FILE REFERENCE: 06087.0200.CPUS01
 / CURRENT APPLICATION NUMBER: US/10/310.914A
 / CURRENT FILING DATE: 2002-12-06
 / NUMBER OF SEQ ID NOS: 1388402
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 638790
 / LENGTH: 21
 / TYPE: RNA
 / ORGANISM: Human
 US-10-310-914A-638790

Alignment Scores:

Pred. No.:	380	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-310-914A-638790 (1-21)

Cy 273 LeuValAlaGlnProArgArg 279 ✓

Db 21 CTAGTGGCCAGCCCCGACGA 1

RESULT 3

US-10-310-914A-814306
 / Sequence 814306, Application US/10310914A
 / Publication No. US20060003322A1
 / GENERAL INFORMATION:
 / APPLICANT: Bentwich, Isaac
 / APPLICANT: Shlier, Kyuzat
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 / TITLE OF INVENTION: uses thereof
 / FILE REFERENCE: 06087.0200.CPUS01
 / CURRENT APPLICATION NUMBER: US/10/310.914A
 / CURRENT FILING DATE: 2002-12-06
 / NUMBER OF SEQ ID NOS: 1388402
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 814306
 / LENGTH: 21
 / TYPE: RNA
 / ORGANISM: Human
 US-10-310-914A-814306

Alignment Scores:

Pred. No.:	380	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-310-914A-814306 (1-21)

Cy 150 Q1YAlaG1YAlaG1YArgG1Y 156 ✓

Db 1 GGUUGUGUGUGUGUGUGUGUGU 21

RESULT 4

US-10-310-914A-1320691/C
 / Sequence 1320691, Application US/10310914A

/ Publication No. US20060003322A1

/ GENERAL INFORMATION:
 / APPLICANT: Bentwich, Isaac
 / APPLICANT: Shlier, Kyuzat
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 / TITLE OF INVENTION: uses thereof
 / FILE REFERENCE: 06087.0200.CPUS01
 / CURRENT APPLICATION NUMBER: US/10/310.914A
 / CURRENT FILING DATE: 2002-12-06
 / NUMBER OF SEQ ID NOS: 1388402
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 1320691
 / LENGTH: 21
 / TYPE: RNA
 / ORGANISM: Human
 US-10-310-914A-1320691

Alignment Scores:

Pred. No.:	380	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-310-914A-1320691 (1-21)

Cy 21 ArgLeuG1YAlaG1YArgG1Y 27 ✓

Db 21 AGGTTGGGGCGCGAGAGGGG 1

RESULT 5

US-10-310-914A-56004/C
 / Sequence 56004, Application US/10310914A
 / Publication No. US20060003322A1
 / GENERAL INFORMATION:
 / APPLICANT: Bentwich, Isaac
 / APPLICANT: Shlier, Kyuzat
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 / TITLE OF INVENTION: uses thereof
 / FILE REFERENCE: 06087.0200.CPUS01
 / CURRENT APPLICATION NUMBER: US/10/310.914A
 / CURRENT FILING DATE: 2002-12-06
 / NUMBER OF SEQ ID NOS: 1388402
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 56004
 / LENGTH: 22
 / TYPE: RNA
 / ORGANISM: Human
 US-10-310-914A-56004

Alignment Scores:

Pred. No.:	397	Length:	22
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-310-914A-56004 (1-22)

Cy 495 ArgArgAlaG1YArgG1YArgG1Y 501

Db 21 AGGAGGCTGAAAGGAGGCA 1

RESULT 6

US-10-310-914A-374833
 / Sequence 374833, Application US/10310914A
 / Publication No. US20060003322A1
 / GENERAL INFORMATION:
 / APPLICANT: Bentwich, Isaac
 / APPLICANT: Shlier, Kyuzat
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

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/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 374833
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-374833

Alignment Scores:
Pred. No.: 397
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.05%
DB: 6
Length: 22
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-374833 (1-22)

Qy 150 G1YAlAG1YAlAG1YArgGly 156
Db 2 GGGGCGAGGGCGCGCGCGCGG 22

RESULT 7
US-10-310-914A-626661
/ Sequence 626661, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 626661
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-626661

Alignment Scores:
Pred. No.: 397
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.05%
DB: 6
Length: 22
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-626661 (1-22)

Qy 150 G1YAlAG1YAlAG1YArgGly 156
Db 2 GGGGCGAGGGCGCGCGCGG 22

RESULT 8
US-10-310-914A-1064918/c
/ Sequence 1064918, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402

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/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1064918
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1064918

Alignment Scores:
Pred. No.: 397
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.05%
DB: 6
Length: 22
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1064918 (1-22)

Qy 160 ArgValProPheSerSerPro 166
Db 22 AGGTCACACCGTCTCCGCA 2

RESULT 9
US-10-310-914A-1205143/c
/ Sequence 1205143, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1205143
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1205143

Alignment Scores:
Pred. No.: 397
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.05%
DB: 6
Length: 22
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1205143 (1-22)

Qy 156 G1YAlAaPProAryValPro 162
Db 21 GGAGCGAGCCCTAGGTCGCC 1

RESULT 10
US-10-310-914A-42890
/ Sequence 42890, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 42890
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human

```

US-10-310-914A-42890

Alignment Scores:

Pred. No.: 414 Length: 23
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-42890 (1-23)

QY 150 G1YALAGIYALAGIYARGIY 156
 DB 3 GGGCGCGCGCGCGCGCGCGCG 23

RESULT 11

US-10-310-914A-374831
 Sequence 374831, Application US/10310914A
 Publication No. US20060003322A1
 GENERAL INFORMATION:
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shlier, Kiyazat
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 FILE REFERENCE: 06087.0200.CPUS01
 CURRENT APPLICATION NUMBER: US/10/310,914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: Patent in version 3.3
 SEQ ID NO 374831
 LENGTH: 23
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-374831

Alignment Scores:

Pred. No.: 414 Length: 23
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-374831 (1-23)

QY 150 G1YALAGIYALAGIYARGIY 156
 DB 1 GGGCGCGCGCGCGCGCGCGCG 21

RESULT 12

US-10-310-914A-482394
 Sequence 482394, Application US/10310914A
 Publication No. US20060003322A1
 GENERAL INFORMATION:
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shlier, Kiyazat
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 FILE REFERENCE: 06087.0200.CPUS01
 CURRENT APPLICATION NUMBER: US/10/310,914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: Patent in version 3.3
 SEQ ID NO 482394
 LENGTH: 23
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-482394

Alignment Scores:

Pred. No.: 414 Length: 23
 Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-482394 (1-23)

QY 18 ArgLeuLeuArgLeuGlyAla 24
 DB 3 AGGCUUCUACGCCUUGGGGCG 23

RESULT 13

US-10-310-914A-542344/c
 Sequence 542344, Application US/10310914A
 Publication No. US20060003322A1
 GENERAL INFORMATION:
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shlier, Kiyazat
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 FILE REFERENCE: 06087.0200.CPUS01
 CURRENT APPLICATION NUMBER: US/10/310,914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: Patent in version 3.3
 SEQ ID NO 542344
 LENGTH: 23
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-542344

Alignment Scores:

Pred. No.: 414 Length: 23
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-542344 (1-23)

QY 184 LeuPheProThrAlaSerAla 190
 DB 23 CTGTTCCCAACGCCAGCGCC 3

RESULT 14

US-10-310-914A-815510/c
 Sequence 815510, Application US/10310914A
 Publication No. US20060003322A1
 GENERAL INFORMATION:
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shlier, Kiyazat
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 FILE REFERENCE: 06087.0200.CPUS01
 CURRENT APPLICATION NUMBER: US/10/310,914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: Patent in version 3.3
 SEQ ID NO 815510
 LENGTH: 23
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-815510

Alignment Scores:

Pred. No.: 414 Length: 23
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-815510 (1-23)

Qy 150 GYALAGLYALAGLYARGG 156
 |||||
 Db 21 GGTGCGAGAGCTGCGCGAGGT 1

RESULT 15

US-10-310-914A-1320692/c
 / Sequence 1320692, Application US/10310914A
 / Publication No. US20060003322A1
 / GENERAL INFORMATION:
 / APPLICANT: Benwich, Isaac
 / APPLICANT: Shiler, Kuzac
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 / FILE OF INVENTION: uses thereof
 / FILE REFERENCE: 06087,0200,CPUS01
 / CURRENT APPLICATION NUMBER: US/10/310,914A
 / NUMBER OF SEQ ID NOS: 138402
 / SOFTWARE: Patent version 3.3
 / SEQ ID NO 1320692
 / LENGTH: 23
 / TYPE: RNA
 / ORGANISM: Human
 US-10-310-914A-1320692

Alignment Scores:

Pred. No.:	414	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-310-914A-1320692 (1-23)

Qy 20 LeuArgLeuGlyAlaGlu 26
 |||||
 Db 23 CTAAGTTGGGCGCGAGAG 3

Search completed: January 12, 2006, 13:59:49
 Job time : 295 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2006, 10:25:28 / Search time 8980 Seconds

(without alignments)
4088.375 Million cell updates/sec

Title: US-10-048-046-2

Perfect score: 664

Sequence: 1 MERBEGKQSPQPMGRLL.....VKAHAMKFNHCQETRFKN 664

Scoring matrix: BLOSUM62

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Ygapop 60.0, Ygapext 60.0
Pgapop 6.0, Pgapext 7.0
Delop 6.0, Delext 7.0

Searched: 79147668 seqs, 27645789525 residues

Post-processing: Listing first 45 summaries

Total number of hits satisfying chosen parameters: 87479736

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Command line parameters:

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-ALIGN=15 -MODE=LOCAL -OUTFMT=prco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50
-USER=US10048046@cgn2_1_7336 @runat.10012006.122940.24149 -NCPU=6 -ICPU=3
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-FDB_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Pending_Patents_NA_Main:

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4: /cgn2_6/prodata/1/pna/US0964_COMB.seq.*
5: /cgn2_6/prodata/1/pna/US0965_COMB.seq.*
6: /cgn2_6/prodata/1/pna/US0966_COMB.seq.*
7: /cgn2_6/prodata/1/pna/US0967_COMB.seq.*
8: /cgn2_6/prodata/1/pna/US0968_COMB.seq.*
9: /cgn2_6/prodata/1/pna/US0969_COMB.seq.*
10: /cgn2_6/prodata/1/pna/US0970_COMB.seq.*
11: /cgn2_6/prodata/1/pna/US0971_COMB.seq.*
12: /cgn2_6/prodata/1/pna/US0972_COMB.seq.*
13: /cgn2_6/prodata/1/pna/US0973_COMB.seq.*
14: /cgn2_6/prodata/1/pna/US0974_COMB.seq.*
15: /cgn2_6/prodata/1/pna/US0975_COMB.seq.*
16: /cgn2_6/prodata/1/pna/US0976_COMB.seq.*
17: /cgn2_6/prodata/1/pna/US0977_COMB.seq.*
18: /cgn2_6/prodata/1/pna/US0978_COMB.seq.*
19: /cgn2_6/prodata/1/pna/US0979_COMB.seq.*
20: /cgn2_6/prodata/1/pna/US0980_COMB.seq.*
21: /cgn2_6/prodata/1/pna/US0981_COMB.seq.*
22: /cgn2_6/prodata/1/pna/US0982_COMB.seq.*
23: /cgn2_6/prodata/1/pna/US0983_COMB.seq.*
24: /cgn2_6/prodata/1/pna/US0984_COMB.seq.*
25: /cgn2_6/prodata/1/pna/US0985_COMB.seq.*
26: /cgn2_6/prodata/1/pna/US0986_COMB.seq.*
27: /cgn2_6/prodata/1/pna/US0987_COMB.seq.*
28: /cgn2_6/prodata/1/pna/US0988_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.2	25	37	US-09-954-5704-36815 Sequence 36815, A
2	8	1.2	25	37	US-09-954-4278-238351 Sequence 238351, A
3	8	1.2	25	37	US-09-954-4278-238353 Sequence 238353, A
4	8	1.2	25	37	US-09-954-4278-238358 Sequence 238358, A
5	8	1.2	25	37	US-09-954-4278-238359 Sequence 238359, A
6	8	1.2	25	38	US-09-956-604-29770 Sequence 29770, A
7	8	1.2	25	38	US-09-956-604-29770 Sequence 29770, A
8	8	1.2	25	38	US-09-956-604B-29770 Sequence 29770, A

```

9      1.2      25 61 US-10-719-956-88030      Sequence 88030, A
10     1.2      25 66 US-11-036-317-24277      Sequence 24277, A
11     1.2      25 66 US-11-036-317-24394      Sequence 24394, A
12     1.2      25 66 US-11-036-317-60227      Sequence 60227, A
13     1.2      25 66 US-11-036-317-61246      Sequence 61246, A
14     1.2      25 66 US-11-036-317-67592      Sequence 67592, A
15     1.2      25 66 US-11-036-317-108822      Sequence 108822, A
16     1.2      25 66 US-11-036-317-131760      Sequence 131760, A
17     1.2      25 66 US-11-036-317-144618      Sequence 144618, A
18     1.2      25 66 US-11-036-317-153103      Sequence 153103, A
19     1.2      25 66 US-11-036-317-166896      Sequence 166896, A
20     1.2      25 66 US-11-036-317-198348      Sequence 198348, A
21     1.2      25 66 US-11-036-317-233307      Sequence 233307, A
22     1.2      25 66 US-11-036-317-259770      Sequence 259770, A
23     1.2      25 66 US-11-036-317-289125      Sequence 289125, A
24     1.2      25 66 US-11-036-317-320189      Sequence 320189, A
25     1.2      25 66 US-11-036-317-320979      Sequence 320979, A
26     1.2      25 66 US-11-036-317-364136      Sequence 364136, A
27     1.2      25 66 US-11-060-756-62495      Sequence 62495, A
28     1.2      25 66 US-11-060-756-62496      Sequence 62496, A
29     1.2      25 66 US-11-060-756-62497      Sequence 62497, A
30     1.2      25 66 US-11-060-756-62515      Sequence 62515, A
31     1.2      25 66 US-11-060-756-136129      Sequence 136129, A
32     1.2      25 66 US-11-060-756-152376      Sequence 152376, A
33     1.2      25 66 US-11-060-756-179266      Sequence 179266, A
34     1.2      25 66 US-11-060-756-184410      Sequence 184410, A
35     1.2      25 66 US-11-060-756-203366      Sequence 203366, A
36     1.2      25 66 US-11-060-756-203937      Sequence 203937, A
37     1.2      25 66 US-11-060-756-222339      Sequence 222339, A
38     1.2      25 66 US-11-060-756-225655      Sequence 225655, A
39     1.2      25 66 US-11-060-756-236413      Sequence 236413, A
40     1.2      25 66 US-11-060-756-279102      Sequence 279102, A
41     1.2      25 66 US-11-060-756-283375      Sequence 283375, A
42     1.2      25 77 US-60-234-049-37696      Sequence 37696, A
43     1.2      25 79 US-60-427-836-88030      Sequence 88030, A
44     1.2      25 81 US-60-545-213-52495      Sequence 62495, A
45     1.2      25 81 US-60-545-213-62496      Sequence 62496, A

```

ALIGNMENTS

```

RESULT 1
US-09-953-570A-36815/c
/ Sequence 36815, Application US/09953570A
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
/ FILE REFERENCE: 3110.1
/ CURRENT APPLICATION NUMBER: US/09/953,570A
/ PRIOR FILING DATE: 2001-09-13
/ PRIOR APPLICATION NUMBER: 60/332,638
/ PRIOR FILING DATE: 2000-09-14
/ NUMBER OF SEQ ID NOS: 138410
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 36815
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-36815

```

Alignment Scores:

```

Pred. No.: 716      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 37      Gaps: 0

```

US-10-048-046-2 (1-664) x US-09-953-570A-36815 (1-25)

```

QY 77 ThirstTherapyThyThyThy 84
DB 24 ACCTTACCAAGTGGCACCGTGAAT 1

```

```

RESULT 2
US-09-954-427A-238351
/ Sequence 238351, Application US/09954427A
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
/ FILE REFERENCE: 3112.1
/ CURRENT APPLICATION NUMBER: US/09/954,427A
/ PRIOR FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,166
/ NUMBER OF SEQ ID NOS: 420907
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 238351
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus Norvegicus
US-09-954-427A-238351

```

```

Alignment Scores:
Pred. No.: 716      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 37      Gaps: 0

```

US-10-048-046-2 (1-664) x US-09-954-427A-238351 (1-25)

```

QY 304 CytelleleCysGlnApplenu 311
DB 2 TGATCATCTGTCAAGACCTCTG 25

```

```

RESULT 3
US-09-954-427A-238353
/ Sequence 238353, Application US/09954427A
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
/ FILE REFERENCE: 3112.1
/ CURRENT APPLICATION NUMBER: US/09/954,427A
/ PRIOR FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,166
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 420907
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 238353
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus Norvegicus
US-09-954-427A-238353

```

Alignment Scores:

```

Pred. No.: 716      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 37      Gaps: 0

```

US-10-048-046-2 (1-664) x US-09-954-427A-238353 (1-25)

```

QY 302 LeuthrCyselleleCysGlnasp 309
DB 2 CTACCTTATCATCTGTCAAGAC 25

```

```

RESULT 4
US-09-954-427A-238358
/ Sequence 238358, Application US/09954427A
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome

```

```

/ FILE REFERENCE: 3112.1
/ CURRENT APPLICATION NUMBER: US/09/954,427A
/ CURRENT FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,166
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 420907
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 238358
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus Norvegicus
/ US-09-954-427A-238358

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-10-048-046-2 (1-664) x US-09-954-427A-238358 (1-25)

QY 300 GIUthrlaethrCysilleyCys 307
DB 2 GAAGACCTAACGTCATCATCTCT 25

RESULT 5
US-09-954-427A-238359
/ Sequence 238359, Application US/09954427A
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
/ FILE REFERENCE: 3112.1
/ CURRENT APPLICATION NUMBER: US/09/954,427A
/ CURRENT FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,166
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 420907
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 238359
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus Norvegicus
/ US-09-954-427A-238359

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-10-048-046-2 (1-664) x US-09-954-427A-238359 (1-25)

QY 294 LyePtoaplyMecjluqluthr 301
DB 2 AAACGACGACAGATGAGAGAGACA 25

RESULT 6
US-09-956-604-29770/C
/ Sequence 29770, Application US/09956604
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Becherichia coli
/ FILE REFERENCE: 3117.1
/ CURRENT APPLICATION NUMBER: US/09/956,604
/ CURRENT FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,049
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 141629
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604B-29770

Alignment Scores:

```

```

/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604-29770

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604-29770 (1-25)

QY 462 SerThSerValSerleuthrThr 469
DB 25 AGTAGCTCGTATCGTACTACA 2

RESULT 7
US-09-956-604A-29770/C
/ Sequence 29770, Application US/09956604A
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Becherichia coli
/ FILE REFERENCE: 3117.1
/ CURRENT APPLICATION NUMBER: US/09/956,604A
/ CURRENT FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,049
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 141629
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604A-29770

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604A-29770 (1-25)

QY 462 SerThSerValSerleuthrThr 469
DB 25 AGTAGCTCGTATCGTACTACA 2

RESULT 8
US-09-956-604B-29770/C
/ Sequence 29770, Application US/09956604B
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Becherichia coli
/ FILE REFERENCE: 3117.1
/ CURRENT APPLICATION NUMBER: US/09/956,604B
/ CURRENT FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,049
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 141629
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604B-29770

Alignment Scores:

```

Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604B-29770 (1-25)

OY 463 SerTherServalSerleuthrthr 469
DB 25 AGRACGTCGATCGCTACCTACA 2

RESULT 9
US-10-719-956-88030
Sequence 88030, Application US/10719956
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 88030
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-88030

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 61 Gaps: 0

US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25)

OY 303 ThrCySleleleCySglnApeleu 310
DB 1 ACCTGATCATCTGCTCAACCTT 24

RESULT 10
US-11-036-317-24277
Sequence 24277, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 24277
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-24277

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)

OY 48 LeuSerPheProSerAenlyeLeuVal 55
DB 1 CTCCTTCCCGACCATTAACCTG 24

RESULT 11
US-11-036-317-24394
Sequence 24394, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 24394
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-24394

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)

OY 49 SerPheProSerAenlyeLeuVal 56
DB 2 TCTTCCCGACCATTAACCTGCTC 25

RESULT 12
US-11-036-317-60227
Sequence 60227, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60227
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-60227

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)

OY 49 SerPheProSerAenlyeLeuVal 56
DB 1 TCTTCCCGACCATTAACCTGCTC 25

DB 1 TCTTCCCGACGATTAAGTGTG 24

RESULT 13

US-11-036-317-61246

/ Sequence 61246, Application US/11036317

/ GENERAL INFORMATION:

/ APPLICANT: Williams, Alan

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

/ FILE REFERENCE: 3654.1

/ CURRENT APPLICATION NUMBER: US/11/036,317

/ PRIOR FILING DATE: 2005-01-13

/ PRIOR APPLICATION NUMBER: US 60/536,639

/ NUMBER OF SEQ ID NOS: 991174

/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 61246

/ LENGTH: 25

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-036-317-61246

Alignment Scores:

Pred. No.: 716 Length: 25

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.20% Indels: 0

DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)

QY 47 AppleUserPhosphorylase 54

DB 2 GACCTCTCTTCCCGACGATTA 25

RESULT 14

US-11-036-317-67592

/ Sequence 67592, Application US/11036317

/ GENERAL INFORMATION:

/ APPLICANT: Williams, Alan

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

/ FILE REFERENCE: 3654.1

/ CURRENT APPLICATION NUMBER: US/11/036,317

/ PRIOR FILING DATE: 2005-01-13

/ PRIOR APPLICATION NUMBER: US 60/536,639

/ NUMBER OF SEQ ID NOS: 991174

/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 67592

/ LENGTH: 25

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-036-317-67592

Alignment Scores:

Pred. No.: 716 Length: 25

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.20% Indels: 0

DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-67592 (1-25)

QY 46 CytochromeP450 53

DB 1 TGTGACCTCTTCCCGACGAT 24

RESULT 15

US-11-036-317-108822

/ Sequence 108822, Application US/11036317

/ GENERAL INFORMATION:

/ APPLICANT: Williams, Alan

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

/ FILE REFERENCE: 3654.1

/ CURRENT APPLICATION NUMBER: US/11/036,317

/ PRIOR FILING DATE: 2005-01-13

/ PRIOR APPLICATION NUMBER: US 60/536,639

/ NUMBER OF SEQ ID NOS: 991174

/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 108822

/ LENGTH: 25

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-036-317-108822

Alignment Scores:

Pred. No.: 716 Length: 25

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.20% Indels: 0

DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)

QY 388 Aspm1LglnProlyValArg 395

DB 1 GATATGCTGCAACCAAGTCAAG 24

Search completed: January 12, 2006, 13:29:43

Job time : 8982 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2006, 10:27:18 / Search time 130 seconds
(without alignments)
2639.356 Million cell updates/sec

Title: US-10-048-046-2
Perfect score: 664
Sequence: 1 MERPEGKQSPPPQPMGRLL.....VAAHAKMKNICBQTRPRN 664

Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1087749 seqs, 258370665 residues

Total number of hits satisfying chosen parameters: 208730

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPRO_spec/US10048046/runat_10012006_122940_24163/app_query.fasta.1.839
-DB=Pending_Patents_NA_New -OPMT=fastcap -SUFFIX=01lg_gz50.inpn -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNIT8=bits -START=1 -END=1 -MATRIX=01lg
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTPR=prco -NORM=ext -HAPBIZ=500 -MINLEN=50
-USERS=US10048046@cgn_1.1.78@runat_10012006_122940_24163 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUERY -NEG_SSCORES=0 -WAIT -DSBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Pending_Patents_NA_New.*
1: /cgn2_6/pdata/1/pna/PCF_NEW_COMB.seq.*
2: /cgn2_6/pdata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/pdata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/pdata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/pdata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/pdata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/pdata/1/pna/US11_NEW_COMB.seq.*
8: /cgn2_6/pdata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	6	0.9	19	US-10-562-561-562	Sequence 562, App
C 2	6	0.9	19	US-10-562-561-562	Sequence 887, App
C 3	6	0.9	20	US-10-527-552-18	Sequence 18, Appl
C 4	6	0.9	20	US-11-294-621-70	Sequence 70, Appl
C 5	6	0.9	20	US-11-317-798-5513	Sequence 5513, Ap
C 6	6	0.9	21	US-60-742-219-4800	Sequence 4800, Ap
C 7	6	0.9	22	US-11-130-645B-8449	Sequence 8449, Ap
C 8	6	0.9	22	US-11-130-645B-10537	Sequence 10537, A
C 9	6	0.9	22	US-11-130-645B-10712	Sequence 10712, A
C 10	6	0.9	22	US-11-130-645B-13922	Sequence 13922, A

11	6	0.9	22	US-11-130-645B-13924	Sequence 13924, A
12	6	0.9	22	US-11-130-645B-13925	Sequence 13925, A
13	6	0.9	22	US-11-130-645B-16045	Sequence 16045, A
14	6	0.9	23	US-10-515-051-78	Sequence 78, Appl
15	6	0.9	25	US-11-067-260-59	Sequence 59, Appl
16	6	0.9	25	US-11-067-260-61	Sequence 61, Appl
17	6	0.9	25	US-11-067-260-65	Sequence 65, Appl
18	6	0.9	25	US-11-067-260-67	Sequence 67, Appl
19	6	0.9	25	US-11-067-260-92	Sequence 92, Appl
C 20	6	0.9	25	US-11-315-777-1	Sequence 1, Appl1
C 21	6	0.9	25	US-11-315-873-1	Sequence 12, Appl
C 22	6	0.9	25	US-60-735-352-12	Sequence 37, Appl
C 23	6	0.9	26	US-10-149-553B-17	Sequence 1077, Ap
C 24	6	0.9	27	US-11-301-360-1077	Sequence 5547, Ap
C 25	6	0.9	29	US-11-317-798-5547	Sequence 2441, Ap
C 26	6	0.9	30	PCT-US05-10912-2441	Sequence 10, Appl
C 27	6	0.9	30	US-60-751-196-10	Sequence 15, Appl
C 28	6	0.9	30	US-60-751-196-15	Sequence 10, Appl
C 29	6	0.9	31	US-11-262-284-10	Sequence 2, Appl1
C 30	6	0.9	33	US-11-275-346-2	Sequence 7, Appl
C 31	6	0.9	34	US-11-067-260-75	Sequence 3675, Ap
C 32	6	0.9	35	US-11-317-798-3675	Sequence 13, Appl
C 33	6	0.9	35	US-09-142-471D-13	Sequence 5306, Ap
C 34	6	0.9	35	US-11-067-260-111	Sequence 106, Ap
C 35	6	0.9	35	US-11-067-260-106	Sequence 73, Appl
C 36	6	0.9	38	US-11-067-260-73	Sequence 63, Appl
C 37	6	0.9	39	US-11-067-260-73	Sequence 69, Appl
C 38	6	0.9	41	US-11-067-260-63	Sequence 87, Appl
C 39	6	0.9	41	US-11-067-260-67	Sequence 102, App
C 40	6	0.9	41	US-11-067-260-77	Sequence 71, Appl
C 41	6	0.9	41	US-11-067-260-87	Sequence 94, Appl
C 42	6	0.9	41	US-11-067-260-87	
C 43	6	0.9	42	US-11-199-820A-102	
C 44	6	0.9	42	US-11-067-260-71	
C 45	6	0.9	42	US-11-067-260-94	

ALIGNMENTS

RESULT 1
US-10-562-561-562/c
Sequence 562, Application US/10562561
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: McSwigen, James
TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using
FILE REFERENCE: 400/166 (MBH02-728-G)
CURRENT APPLICATION NUMBER: US/10/562, 561
PRIOR FILING DATE: 2005-12-28
PRIOR APPLICATION NUMBER: US 10/607933
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 09/930423
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: PCT/US03/04710
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 10/205309
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693059
PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: US 10/444853
PRIOR FILING DATE: 2003-05-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1904

SOFTWARE: PatentIn version 3.3
SEQ ID NO 562
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sRNA sense
US-10-562-561-562

Alignment Scores:
Pred. No.: 885 Length: 19
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-10-562-561-562 (1-19)

QY 193 ThrgUpProSarProA1a 198
DB 19 ACAGAGCCAGCCCTCT 2

RESULT 2
US-10-562-561-887
Sequence 887, Application US/10562561
GENERAL INFORMATION:
APPLICANT: Sigma Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Belgelmen, Leonid
TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using
TITLE OF INVENTION: Short Interfering Nucleic Acid (siRNA)
FILE REFERENCE: 400/166 (WAB02-728-G)
CURRENT APPLICATION NUMBER: US/10/562,561
PRIOR FILING DATE: 2005-12-28
PRIOR APPLICATION NUMBER: US 10/607933
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 09/930423
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: PCT/US03/04710
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 10/205309
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693059
PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: US 10/444853
PRIOR FILING DATE: 2003-05-23
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1904
SOFTWARE: PatentIn version 3.3
SEQ ID NO 887
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
US-10-562-561-887

Alignment Scores:
Pred. No.: 885 Length: 19
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-10-562-561-887 (1-19)

QY 193 ThrgUpProSarProA1a 198
DB 1 ACAGAGCCAGCCCTCT 18

RESULT 3
US-10-527-552-18
Sequence 18, Application US/10527552
GENERAL INFORMATION:
APPLICANT: Sandoz GmbH
TITLE OF INVENTION: Process for production of cephalosporin C
FILE REFERENCE: IB/G-32677A/BCK
CURRENT APPLICATION NUMBER: US/10/527,552
CURRENT FILING DATE: 2005-03-11
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-10-527-552-18

Alignment Scores:
Pred. No.: 926 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-10-527-552-18 (1-20)

QY 208 SerGlyGlyGlyGly 213
DB 1 TCGGAGGTGGAGGATT 18

RESULT 4
US-11-294-621-70/c
Sequence 70, Application US/11294621
GENERAL INFORMATION:
APPLICANT: BELL, DAPHNE WINIFRED
APPLICANT: HARR, DANIEL A.
APPLICANT: JARNE, PAST ANTERO
APPLICANT: JOHNSON, BRUCE E.
APPLICANT: LYNCH, THOMAS J.
APPLICANT: MEYERSON, MATTHEW
APPLICANT: PAEZ, JUAN GUILHERMO
APPLICANT: SELLERS, WILLIAM R.
APPLICANT: SETTLEMEN, JEFFREY E.
APPLICANT: SORBELLA, NAFAELIA
TITLE OF INVENTION: METHOD TO DETERMINE RESPONSIVENESS OF CANCER TO
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR TARGETING
FILE REFERENCE: 030258-055147
CURRENT APPLICATION NUMBER: US/11/294,621
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: PCT/US05/010645
PRIOR FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: 60/558,218
PRIOR FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: 60/561,095
PRIOR FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/565,753
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60/565,985
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60/574,035
PRIOR FILING DATE: 2004-05-25
PRIOR APPLICATION NUMBER: 60/577,916

/ PRIOR FILING DATE: 2004-06-07
 / PRIOR APPLICATION NUMBER: 60/592,287
 / PRIOR FILING DATE: 2004-07-29
 / NUMBER OF SEQ ID NOS: 762
 / SOFTWARE: PatentIn Ver. 3.3
 / SEQ ID NO 70
 / LENGTH: 20
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-11-294-621-70

Alignment Scores:

Pred. No.:	926	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-294-621-70 (1-20)

Qy 77 Thrserrhserrgylthr 82

Db 19 ACTTCACCTCGGCACA 2

RESULT 5

/ Sequence 5513, Application US/11317798
 / GENERAL INFORMATION:

/ APPLICANT: Lofton-Day, Cathy; Model, Fabiani, Sledziewski,
 / APPLICANT: Andrew; Rujan, Tamas; Lewin, Joern; Distler, Jergen
 / TITLE OF INVENTION: Methods and nucleic acids for the analysis of colon cell
 / FILE REFERENCE: 47675-174
 / CURRENT APPLICATION NUMBER: US/11/317,798
 / CURRENT FILING DATE: 2005-12-23
 / PRIOR APPLICATION NUMBER: US 10/603,138
 / PRIOR FILING DATE: 2003-06-23
 / PRIOR APPLICATION NUMBER: PCT/US04/20336
 / PRIOR FILING DATE: 2004-06-23
 / PRIOR APPLICATION NUMBER: US 10/602,494
 / PRIOR FILING DATE: 2003-06-23
 / PRIOR APPLICATION NUMBER: EP 04090175.3
 / PRIOR FILING DATE: 2004-05-06
 / PRIOR APPLICATION NUMBER: EP 04090072.2
 / PRIOR FILING DATE: 2004-02-27
 / NUMBER OF SEQ ID NOS: 14624
 / SEQ ID NO 5513
 / LENGTH: 20
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE: bisulfite treated
 / OTHER INFORMATION: nucleic acid for analysis of methylation status of SEQ ID NO: 45
 US-11-317-798-5513

Alignment Scores:

Pred. No.:	926	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-317-798-5513 (1-20)

Qy 394 VALARGARSGerPhaser 399

Db 1 GTGACCTTCCTTTTCG 18

RESULT 6

/ Sequence 4800, Application US/60742219
 / GENERAL INFORMATION:

/ APPLICANT: Belouchi, Abdelmajid
 / APPLICANT: Raelson, John Verner
 / APPLICANT: Bradley, Walter Edward
 / APPLICANT: Baguin, Bruno
 / APPLICANT: Nguyen-Huu, Quynh
 / APPLICANT: Croteau, Pascal
 / APPLICANT: Allard, Rene
 / APPLICANT: Little, Randall David
 / APPLICANT: Ketch, Tim
 / APPLICANT: Cousineau, Johanne
 / APPLICANT: Berdevegh, Paul Van
 / APPLICANT: Segal, Jonathan
 / TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis
 / FILE REFERENCE: 306522-2000
 / CURRENT APPLICATION NUMBER: US/60/742,219
 / CURRENT FILING DATE: 2005-12-05
 / NUMBER OF SEQ ID NOS: 7303
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 4800
 / LENGTH: 21
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-60-742-219-4800

Alignment Scores:

Pred. No.:	967	Length:	21
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	8	Gaps:	0

US-10-048-046-2 (1-664) x US-60-742-219-4800 (1-21)

Qy 243 SerSerLeugluProgn 248

Db 3 TCCTCCTTGGAGCCAG 20

RESULT 7

/ Sequence 8449, Application US/1130645B
 / GENERAL INFORMATION:

/ APPLICANT: ROSETTA GENOMICS LTD
 / TITLE OF INVENTION: MICRONAS AND USES THEREOF
 / FILE REFERENCE: 06087,0202,CPUS13
 / CURRENT APPLICATION NUMBER: US/11/130,645B
 / CURRENT FILING DATE: 2005-05-16
 / NUMBER OF SEQ ID NOS: 76016
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 8449
 / LENGTH: 22
 / TYPE: RNA
 / ORGANISM: Homo sapiens
 US-11-130-645B-8449

Alignment Scores:

Pred. No.:	1,016+03	Length:	22
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-130-645B-8449 (1-22)

Qy 3 ArgProglugluGlyLe 8

Db 4 AGCCAGAGAGAGAGAG 21

RESULT 8

/ Sequence 10537, Application US/1130645B
 / GENERAL INFORMATION:

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/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 10537
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-10537

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-10537 (1-22)

Qy 195 ProSepproAlaGlyArg 200
Db 5 CCCUCUCCUGGCGGCGA 22

RESULT 9
US-11-130-645B-10712/c
/ Sequence 10712, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 10712
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-10712

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-10712 (1-22)

Qy 452 GYAlaProGlnAlaLeu 457
Db 22 GCGGCTCCCAAGGCGCTC 5

RESULT 10
US-11-130-645B-13922
/ Sequence 13922, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 13922
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens

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US-11-130-645B-13922

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-13922 (1-22)

Qy 368 ApLySerArgSerGlu 373
Db 5 GAUAAGUCAGGUCUGAA 22

RESULT 11
US-11-130-645B-13924
/ Sequence 13924, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 13924
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-13924

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-13924 (1-22)

Qy 368 ApLySerArgSerGlu 373
Db 5 GAUAAGUCAGGUCUGAA 22

RESULT 12
US-11-130-645B-13926
/ Sequence 13926, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 13926
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-13926

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-13926 (1-22)

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Qy 368 ApplySerArgSerjlu 373
 |||||
 Db 5 GAUAGUCAGGUCUCAA 22

RESULT 13

US-11-130-645B-16045
 / Sequence 16045, Application US/11130645B
 / GENERAL INFORMATION:
 / APPLICANT: ROSETTA GENOMICS LTD
 / TITLE OF INVENTION: MICRONAS AND USBS THEREOF
 / FILE REFERENCE: 06087.0202.CPUS13
 / CURRENT APPLICATION NUMBER: US/11/130,645B
 / PENDING FILING DATE: 2005-05-16
 / NUMBER OF SEQ ID NOS: 760616
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 16045
 / LENGTH: 22
 / TYPE: RNA
 / ORGANISM: Homo sapiens
 / OTHER INFORMATION: US-11-130-645B-16045

Alignment Scores:

Pred. No.:	1.01e+03	Length:	22
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-130-645B-16045 (1-22)

Qy 161 ValProProSerSerPro 166
 |||||
 Db 5 GUCCUCCUCCAGUCUA 22

RESULT 14

US-10-515-051-78
 / Sequence 78, Application US/10515051
 / GENERAL INFORMATION:
 / APPLICANT: OHNO, Ryo-ozo
 / APPLICANT: TSURUO, Takashi
 / APPLICANT: NAKAMURA, Yusuke
 / TITLE OF INVENTION: METHOD FOR JUDGING SENSIBILITY TO IMATINIB
 / FILE REFERENCE: 0760-0342PUS1
 / CURRENT APPLICATION NUMBER: US/10/515,051
 / PENDING FILING DATE: 2004-11-19
 / PRIOR APPLICATION NUMBER: PCT/JP03/06330
 / PENDING FILING DATE: 2003-05-21
 / NUMBER OF SEQ ID NOS: 154
 / SEQ ID NO 78
 / LENGTH: 23
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Oligonucleotide reverse primer used for amplifying human CTS6 cDN
 / OTHER INFORMATION: A
 / OTHER INFORMATION: US-10-515-051-78

Alignment Scores:

Pred. No.:	1.05e+03	Length:	23
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-515-051-78 (1-23)

Qy 17 GlyArgLeuLeuArgLeu 22
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 Db 4 GGACGTTTATTAAGGCTC 21

RESULT 15
 US-11-067-260-59
 / Sequence 59, Application US/11067260
 / GENERAL INFORMATION:
 / APPLICANT: Arico, Maria
 / TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
 / FILE REFERENCE: 223002099501
 / CURRENT APPLICATION NUMBER: US/11/067,260
 / PENDING FILING DATE: 2005-02-25
 / PRIOR APPLICATION NUMBER: 10/220,480
 / PRIOR FILING DATE: 2002-08-28
 / PRIOR APPLICATION NUMBER: PCT/IB01/00420
 / PRIOR FILING DATE: 2001-02-28
 / NUMBER OF SEQ ID NOS: 121
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 59
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: fu (961) -741 (MC58) -His Pvd
 / OTHER INFORMATION: US-11-067-260-59

Alignment Scores:

Pred. No.:	1.13e+03	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-067-260-59 (1-25)

Qy 207 GlySerGlyGlyGlyGly 212
 |||||
 Db 4 GGATCCGAGGAGGAGTGT 21

Search completed: January 12, 2006, 13:31:58
 Job time : 130 secs